

Amendments to the specification:

On page 15, line 34, please replace the original paragraph with the following amended paragraph:

Figure 16 (SEQ ID NOS: 66 - 92) shows conservation between anchor regions of polypeptides of the invention.

On page 17, line 32, please replace the original paragraph with the following amended paragraph:

***Escherichia coli***

Polypeptides were found in pathogenic strains of *E. coli*, including enteropathogenic (EPEC), enteroaggregative (EAEC), enterohemorrhagic (EHEC) and uropathogenic (UPEC) strains. Furthermore, a polypeptide almost identical to those of the EHEC and EPEC strains was found in the K1 strain, which is a capsulated *E. coli* strain responsible for neonatal meningitis. The K1 sequence (SEQ ID NO: 93) aligns with NadA (SEQ ID NO: 94) as follows:

	100	110	120	130	140	150	
k1.pep	TGVVQIPARYQSMINARQSAVTDAQQTQITEQQAQIVATQKTLAATGDTQNTAHYQEMIN						
				::     ::     ::     ::   ::   ::   ::			
NadA.pep	DAALADTDAALDETTNALNKLGENITTFABETKTNIVKIDEKLEAVADTVD--KHAEAFN						
	130	140	150	160	170	180	
	160	170	180	190	200	210	
k1.pep	ARLAAQNEANQRTTTEQGQKMNALTTDVAAQQQKERAQYDKQMQLAQKSVQAHEQIESL						
	: ::    ::::   : ::   : ::   : ::   : ::   : ::   : ::						
NadA.pep	DIADSLDETNT--TKADEAVKTANEAKQTAEETKQNVDAKVAETAAGKAEAAAGTANTA						
	190	200	210	220	230	240	
	220	230	240	250	260	270	
k1.pep	RQDSAQTQQQLTNTQKRVADNSQQINTLNNHFDLSLKNEVEDNRKEANAGTASAIASQP						
	: : : : ::  : :   : :      : :   :      :      :      :      :						
NadA.pep	ADKAEAVAAKVTDIKADIATNKADIAKNSARIDSLDKNVANLRKETROGLAEQAALSGLF						
	250	260	270	280	290	300	
	280	290	300	310	320	330	
k1.pep	QVKTGDMVMVSAGAGTFNGESAVSVGTSFNAGTHTVLKAGISADTQSDFGAGVGVGYSF						
	: :   :    :   :       :    :   : :    :    :   :   :   :   :   :						
NadA.pep	QPYNVGRFENVTAAVGGYKSESAVAIGTGFRFTENFAAKAGVAVGTSSGSSAAYHVGVNIEW						
	310	320	330	340	350	360	

24.4% identity in 209 aa overlap

On page 20, line 1, please replace the original paragraph with the following amended paragraph:

***Haemophilus***

An incomplete NadA homolog was found in Brazilian purpuric fever (BPF) *Haemophilus influenzae* isolates {156}. This polypeptide has been named HadA. ~~NadA and HadA~~ HadA (SEQ ID NO: 95) and NadA (SEQ ID NO: 96) align as follows:

		10	20	30	40	
HadA.pep		MKRNLKQSVIAVLIGGTTVSNYALAAQAQAQVKKDELSELKKQVKEM-				
				::    ::	:	:  ::  :::
NadA.pep	KTVNENKQNVDAKVKAASEIEKLT	KLADTDAALADTDAALDET	TNALNKLGENIT	TFA		
	100	110	120	130	140	150
	50	60	70	80	90	100
HadA.pep	DAAIDGILDDNIAYEAEVDAKLDOHSAALGRHTNRLNNLKTIAEKAKGDSSEALDKIEAL					
	:	:	: :	:	: :	: :  : :
NadA.pep	EETKTNIVKIDEKLEAVADT	VDKHAEAFNDIADSLDET	TNTKADEAVKTANEAKQTAEET			
	160	170	180	190	200	210
	110	120	130	140	150	160
HadA.pep	EEQNDEFLADITALEEGVDGLDDDIAGIQDNISD----IEDDINQNSADIATNTAAIATH					
	:	:		:	:	:
NadA.pep	KQNV	DAKAAETAA	GKAEAAAGTANTAADKAE	AAKVT	DIKADIATNKADI	AKN
	220	230	240	250	260	270
	170	180	190	200	210	220
HadA.pep	TQRLDNLDNRVNNLNKDLKRGALAAQALNGLFQPYNVGKLNLTAAVGGYKSQTAVAVG					
	:	: : :	:	: :	:	: : : : : : : : : : :
NadA.pep	SARIDSLDKNVANLRKETRQGLAEQAALSGLFQPYNVGRFNVTA	AAVGGYKSES	AVAIGTG			
	280	290	300	310	320	330
NadA.pep	FRFTENFAAKAGVAVGTSSGSSAAYHVGVN					
	340	350	360			

On page 21, line 5, please replace the original paragraph with the following amended paragraph:

~~NadA and the~~ The *H. actinomycescomitans* (SEQ ID NO: 97) and the NadA (SEQ ID NO: 98) sequence align as follows:

[illegible]

37.0% identity in 284 aa overlap

On page 21, line 6, please replace the original paragraph with the following amended paragraph:

NadA and the The *H.somnus* (SEQ ID NO: 99) and the NadA (SEQ ID NO: 100) sequence align as follows:

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          90          100          110          120          130          140
H.somnus.pep EVIKGWNEVKSLPRIDGNGKDKQTKDQIAMLRITVDNTEKLGRIVSTNIEDIKNLKKELY
              | | | : : : : : | : |
NadA.pep      MSMKHFP SKVLTTAILATFCSGALAATSDD--DVKKAATVAIVAAYNNGQEIIN
              10          20          30          40          50

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      150      160      170      180      190
H.somnus.pep GF-----VEDVNES---EARNISRIDENEKDIKNL--KKELYDFVEDVNESEARNISRID
              || : ||::: :: : | : ||::| || : :::: ||::: :::
NadA.pep     GFKAGETIYDIGEDGTITQKDATAADVEADDFKGLGLKKVVTNLTKTVNENKQNVDAKVK
              60      70      80      90      100     110

      200      210      220      230      240      250
H.somnus.pep ENEKDINTLK-ELMDED--LNSVLTQIEDVKLTQDVNDNVNLAFAEEINGNAQKFDTAIE
              |::|| : || | | | : : :::: :: : ::||:: || : | || : |
NadA.pep     AAESEIEKLTTKLADTDAALADTDAALDETTNALNKLGENITTFAEETKTNIVKIDEKLE
              120     130     140     150     160     170

      260      270      280      290      300      310
H.somnus.pep GLTSGLSDLQAKVDANKQETEDDIADNAKAIHSNTKGIKNTKDIRDLDTKTKQMLENDK
              :::: || : | : ||||: :::: :|::: :: : |||
NadA.pep     AVAD-----TVDKHA-EAFNDIADSLDETNTKADEAVKTANEAKQTAEETKQ-----
              180     190     200     210

      320      330      340      350      360      370
H.somnus.pep NLMTGLESLATETSKGFERFDVKTTQQLDQAVANVVGVRVDITEQAIRQNTAGLVNVNKRVD
              | : : :: | ::| : : | : | | ::::| : | | | :: : | : |
NadA.pep     NVDAKVKAETAAGKAEAAAAGTANTAADKAEA-VAKVTDIKADIATNKADIKN SARID
              220     230     240     250     260     270

      380      390      400      410      420
H.somnus.pep TLDKN-----TKAGIASAVALGMLPQSTAPGKSLVSLGVGHHRGQSATAIGVSSMSSN
              :||| | : || : ||: | | | : | : || ::::||:| | | :: :
NadA.pep     SLDKNVANLRKETRQGLAEQAALSGLFQPYNVGRFNVTAAVGGYKSES AVAIG-TGERFT
              280     290     300     310     320     330

      430      440      450
H.somnus.pep GKWVVKGGMSYDTQRHATFGGSSVGFFFN
              ::::|:|:: | : : : ||
NadA.pep     ENFAAKAGVAVGTSSGSSAAYHVG VNYEW
              340     350     360
```

23.2% identity in 354 aa overlap

~~NadA and the~~ The *H. ducreyi* (SEQ ID NO: 101) and the NadA (SEQ ID NO: 102) sequence align  
as follows:

47.5% identity in 101 aa overlap

An alignment of ~~NadA and HadA~~ (SEQ ID NO: 103) and NadA (SEQ ID NO: 104) (39.5% identity in 243 aa overlap) is given below:

[illegible]

On page 25, line 8 please replace the original paragraph with the following amended paragraph:

Immediately downstream of *hadA* is a gene encoding a hypothetical protein (SEQ ID NOS: 53 & 54), which is frame-shifted in strain KW20 and absent from all other *Haemophilus* strains tested. The closest database match for this protein is ZP\_00132218. 1, the histone acetyltransferase HPA2 and related acetyltransferases from *Haemophilus somnus* 2336 (SEQ ID NO: 55):

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Length = 168

Score = 276 bits (707), Expect = 9e-74  
Identities = 139/168 (82%), Positives = 149/168 (88%)

(SEQ ID NO: 105)

Query: 1 MINENLAYLSVLPLEDVKIERSSFSCSVEPLENYFHKYVSQDVKKGLAKCFVLINAQPSR 60

(SEQ ID NO: 106)

MINENL YLSVLPLED+ I+R+SFSCSVEPLE YF+KY SQDVKKG+ KCFVLIN Q

(SEQ ID NO: 107)

Sbjct: 1 MINENLPYLSVLPLEDLTIDRNSFSCSVEPLETYFYKYASQDVKKGITKCFVLINKQQFG 60

Query: 61 IVGYTSLALSIPIDIPQERISKGVYPNIPAVLIGRLAIDTNFQKQGYGKFLIADAIH 120

I+GYTSLALSIPIDIPQERISKG+PYPNIPAVL+GRLAIDTNFQ QGYGKFLIADAI+

Sbjct: 61 IIGYTTLSALSIPITDIPQERISKGIPYPNIPAVLVGRLAIDTNFQNGYGKFLIADAIY 120

Query: 121 KIKNATVAATILVVEAKNDASSFYERLGFIEFKEFGGTHRKLIFYPLT 168

KIKNATV A ILVVEAKND A SFY+RLGFIEFK THRKLIFYPLT

Sbjct: 121 KIKNATVGAAILVVEAKNDHAVSFYKRLGFIEFKNLKKTHRKLIFYPLT 168